



# GENE ACTION AND COMBINING ABILITY STUDIES FOR DEVELOPMENT OF HIGH PERFORMING HYBRIDS ACROSS FOUR LOCATIONS IN CHILLI (*CAPSICUM ANNUUM* L.)

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## Abstract

Nature of gene action involved in the inheritance of important quantitative and qualitative traits is elucidated by using six CGMS lines with six restorers in Line × Tester method over four locations, to obtain information for selection of the parents with good *GCA* and crosses with good *SCA* effects. The pooled analysis of variance for combining ability revealed that *SCA* variance was higher in magnitude compared to *GCA* variance for all the characters except days to 50% flowering, plant width, average seed count per fruit, dry chilli yield per plant and pungency, indicating the predominance of non-additive gene action. The *GCA* effects for parents in pooled analysis revealed that, among the lines CM5076B, CM1112B and CM5032B and among the testers NCR3295 and NCR1748 were found to be promising general combiners for dry chilli yield per plot and yield attributing characters. Based on significant *SCA* effects in pooled analysis, eight hybrids CM1162A × NCR1748, CM5032A × NCR3295, CM5076A × NCR1238, CM5032A × NCR1886, CM1008A × NCR1748, CM1008A × NCR3295, CM1037A × NCR1681 and CM1008A × NCR1886 were identified as promising for dry chilli yield per plot and majority of yield attributing characters.

**Key words :** Chilli, cytoplasmic genetic male sterility, gene action, general combining ability, line × tester analysis, specific combining ability and restorer.

**Abbreviations:** *GCA*-General combining ability, *SCA*-Specific combining ability, AVRDC-Asian vegetable research and development centre. CGMS- Cytoplasmic genetic male sterility.

## Introduction

Chilli is one of the commercial vegetable cum spice crop in the most cultivated species from the economic and nutritional point of view in the world (Djian-Caporalino *et al.*, 2006). Second most important solanaceous crop as vegetable in the world after tomato. It is valued for its pungency, which is due to crystalline alkaloid content called capsaicin, present in the placenta of the fruits and colour values of capsanthin. It is generally a self-pollinated crop with chasmogamous flower type, where flowers open only after pollination (Lemma, 1998). However, 2 to 96% out-crossing was observed in open pollination (AVRDC, 2000). Capsicum species are diploid, most having  $2n = 24$  chromosomes. The fruits are consumed fresh, processed or when dried as spice or condiment. India is the largest producer of chilli occupies 36% of world production followed by China 11%. In India, Andhra

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Pradesh occupies 34% (major) area of cultivation for chilli followed by Karnataka, Maharashtra, Madhya Pradesh. Market potential of chilli is around 90 tonnes. The hybrid seed is of Low volume and high value seed market. Share of hybrid seeds has increased up to 40-45% utilization for cultivation.

Cytoplasmic genetic male sterility is a unique parameter important for breeding programmes of many crops as this trait impairs the production of viable pollen from anthers (Kim *et al.*, 2006; Lee *et al.*, 2008). CGMS System applied for producing the  $F_1$  chilli hybrids (Min *et al.*, 2009) as this approach could help to reduce the production cost by 47% compare to the conventional method (Yang *et al.*, 2008). The objective of chilli breeding is to develop high yielding hybrids with high quality parameters and highly tolerance to disease. The line × tester analysis provides a systematic approach for detection of appropriate parents and crosses in terms of

investigated traits (Kempthorne, 1957).

### Materials and Methods

Six CGMS lines *viz.*, CM1008A, CM1037A, CM1112A, CM1162A, CM5032A and CM5076A and six restorer *viz.*, NCR3295, NCR4293, NCR1681, NCR1886, NCR1748 and NCR1238 were planted during *kharif* 2014 at Research station, Medchal, Hyderabad and crossing was performed in line  $\times$  tester fashion to produce 36 hybrids. During *Kharif* 2015, the 36 hybrids along with twelve parents and two check hybrids *viz.*, Indam-5 and Tejaswini were evaluated in RCBD with three replication per location at four different locations *viz.*, Medchal Research Centre, Hyderabad; Parkal Research Centre, Warangal; Cherla Research Centre at Badhrachalam and Mandapadu Research Centre at Guntur. Forty days old seedlings were transplanted with 75  $\times$  45 cm spacing and each entry was planted in one row of 4 m length. All the recommended agronomic cultural and plant protection practices were followed. Observations were recorded on five randomly selected plants in each entry per replication and biometrical data were recorded for days to 50% flowering, plant height, plant width, fruit length, fruit width, number of fruits per plant, average seed count per fruit, thousand seed weight, dry chilli yield per plot, leaf curl virus tolerance, pungency value and capsanthin colour value traits. The mean data obtained over four locations were subjected to line  $\times$  tester analysis, Kempthorne (1957) and Singh and Chaudhary (1979) to estimate the general and specific combining ability effects and their respective variances. The result of pooled analysis of variance over four locations *viz.*, Hyderabad, Warangal, Badhrachalam and Guntur is presented (table 1). Analysis of combining ability was carried out by using Indostat software services, Hyderabad.

### Results and Discussion

The pooled analysis of variance revealed significant differences due to locations for all the characters except LCV, indicating the sufficient diversity among the environment (table 1). The differences among the parents, parents vs crosses and crosses were observed to be significant for all the characters studied except in LCV of parents vs crosses, indicating the existence of wider genetic differences among the parents and crosses. Partitioning of crosses in to lines, testers and lines  $\times$  testers revealed that variance due to lines were significant for all the characters except FW, PUN, ASC and LCV in lines, where as for testers, PH, FL, FW, ASC, TSW were found significant, indicates wide variability existing among

the genotypes. The Interaction due to lines  $\times$  testers were significant for all the traits studied, suggesting that significant contribution of SCA effects towards the variation among the crosses, the results were in accordance with the earlier studies of Hasanuzzaman *et al.* (2012), Payakhapaab *et al.* (2012), Suryakumari *et al.* (2014) and Kranthi Rekha *et al.* (2016).

Interaction effects of parents vs crosses  $\times$  locations, parents  $\times$  locations and crosses  $\times$  locations were significant for all the characters, except for DFF, LCV, CCL & FW in case of (parents vs crosses)  $\times$  locations and DFF & LCV in case of parents vs locations and locations  $\times$  crosses. Further partitioning of crosses  $\times$  locations indicated that the interaction of lines  $\times$  locations showed significant differences for DFF, PH, PW, FL, NFPP & CCL, while testers  $\times$  locations was non-significant for all traits studied, suggesting the sensitivity of *GCA* effects of parents to environmental fluctuations for these characters. Interaction effects of lines  $\times$  testers  $\times$  locations were significant for all the characters studied except LCV, indicates the *SCA* effects of hybrids interacted with the environments for all the characters studied, which are contradictory with the earlier reports of Pandian and Shanmugavelu (1992), Khalil and Hatem (2014). The comparative estimates of variances due to general combining ability (*GCA*) and specific combining ability (*SCA*) revealed the predominance of *SCA* variances in relation to *GCA* variance for the traits DFF, PW, FW, ASC & DCY, which implied that all the characters were predominantly under the control of non-additive gene action, while additive gene action for PH, FL, NFPP, TSW and the results corroborates with the findings of Chaudhary *et al.* (2013), Mendes *et al.* (2014), Kranthi Rekha *et al.* (2016). On the other hand, the magnitude of the interaction for  $\sigma^2$ SCA  $\times$  loc was higher than  $\sigma^2$ GCA  $\times$  loc for all the studied traits except NFPP & LCV. These results indicated that, non-additive gene actions were more sensitive to location differences than additive for all the studied traits. These conclusions are similar to those obtained by Bhagyalakshmi *et al.* (1991), Nandadevi *et al.* (2003), Suryakumari *et al.* (2014) and Kranthi Rekha *et al.* (2016).

Degree of dominance observed to be more than unity for DFF, PW, FW, ASC, DCY, except PH, FL, NFPP, TSW, under study suggesting over-dominance is the major factor for high level of expression of these traits. The results are in accordance with the earlier reports of Payakhapaab *et al.* (2012), Chaudhary *et al.* (2013), Suryakumari *et al.* (2014), Samia Ben Mansoor *et al.* (2015) and Kranthi Rekha *et al.* (2016).

Table 1 : Pooled analysis of variance for combining ability (LxT) for yield and yield attributing attributes for four locations in chili.

Source of variation	DF	DFF	PH	PW	FL	FW	NFPP	ASC	TSW	DCY	LCV	PUN	CCL
Locations	3	51**	682.8**	153.9**	3**	0*	95878.3**	548.8**	0.2**	7164640.5**	0.44	11996.82**	3519.87**
Rep *Loc.	6	3.5	18.6	2.1	0	0	151.6	18.1	0	27411.7	0.16	27.41	33.47
Treatments	47	93.1**	5553.4**	631.6**	35.5**	0.1**	28062.8**	2824.2**	1.1**	9566663**	4.05**	11016.93**	7756.2**
Parents	11	117.4**	7580.7**	1135.7**	47.4**	0.2**	7660**	3155.2**	1**	1146086.9**	6.06**	10668.44**	7316.67**
Parent vs Crosses	1	634.4**	10449.9**	384**	1**	0.1**	578850.6**	31664.1**	3.5**	270711232**	0.67	82498.75**	82654.16**
Crosses	35	70**	4776.4**	480.2**	32.8**	0.1**	18738.3**	1896.2**	1.1**	4751856.5**	3.51**	9084.12**	5754.39 **
Line effect	5	143.5*	8272.9**	1749.9**	39.6**	0.1	91403.2**	821.4	1.1*	4492672.5	4.63	1693.1	16819.6**
Tester effect	5	90.3	20855.7**	167.5	170.7**	0.3**	8290.7	6822.7**	4.7**	6970184.5	5.3	49042.57**	91602.6*
Line * Tester effect	25	51.3**	861.2**	288.8**	3.9**	0.1**	6294.8**	1125.8**	0.4**	4360028**	2.93**	2570.63**	2860.18**
Loc * Parents	33	10.2**	56.5**	14.5**	0.4**	0**	390.2**	80.1**	0*	216205.9**	0.41	358.99**	345.07**
Loc * Parent vs Cross	3	50.6**	865.8**	34**	2.9**	0	24256.6**	126.4**	0.1**	4386790**	0.37	178.2**	80.19
Loc * Crosses	105	14.9**	113**	44.8**	0.4**	0**	6042.8**	161.9**	0.1**	452063.7 **	0.47	415.28 **	399.09 **
Loc * Line effect	15	34.8**	196.8*	78.4*	0.7*	0	28930.5**	255	0.1	589123.6	0.54	676.61	960.88**
Loc * Tester effect	15	11.6	111.2	39.6	0.4	0	2296.3	80.7	0.1	373848.6	0.56	205.75	219.27
Loc * L * T effect	75	11.6**	96.6**	39.1**	0.4**	0**	2214.6**	159.5**	0.1**	440294.8**	0.44	404.92**	322.7**
Error	376	5.2	11.8	4.8	0	0	134.8	17.4	0	63301.6	0.51	38.2	40.91
$\sigma^2$ GCA		1.55	202.12	13.25	1.46	0	689.9	52.82	0.04	78627.4	0.06	<b>351.82</b>	<b>179.78</b>
$\sigma^2$ L*(SCA)		3.82	70.77	23.67	0.32	0.01	510.27	92.23	0.03	357480.97	0.2	<b>211.15</b>	<b>234.53</b>
GCA/SCA variance		0.41	2.86	0.56	4.56	0	1.35	0.57	1.33	0.22	0.3	1.666	0.767
$\sigma^2$ Loc.* GCA		0.99	7.89	3.01	0.03	0	857.88	8.27	0	22846.11	0	22.46	30.23
$\sigma^2$ Loc * L * t(SCAL)		<b>2.06</b>	<b>28.23</b>	<b>11.44</b>	<b>0.11</b>	<b>0</b>	681.03	<b>46.84</b>	<b>0.04</b>	<b>123346.23</b>	-0.04	122.68	92.28
Degree of Dominance		1.11	0.42	0.95	0.33	0.94	0.61	0.93	0.61	1.51	1.27	0.55	0.81

\*: Significant at 5% level; \*\*: significant at 1% level.

**Note:** DFF-days to 50% flowering, PH-Plant height, PW-Plant width, FL-Fruit length, FW-Fruit width, NFPP-Number of fruit per plant, ASC-Average seed count per fruit, TSW –Thousand seed weight, DCY-dry chilli yield per plot, LCV- leaf cult virus tolerance, PUN –Pungency values in Scoville Heat Units mentioned in 1000's, CCL- Capsanthin colour values mentioned in ASTA.

Table 2 : Estimates of general combining ability effects for twelve parents for twelve characters in chilli.

Parents	DFP	PH	PW	FL	FW	NFPP	ASC	TSW	DCY	LCV	PUN	CCL
<b>Lines</b>												
CM1008B	-0.26	-5.33**	-1.55**	0.22**	0.05**	-33.54**	2.05**	-0.04*	-367.81**	-0.22*	-4.14**	-21.93**
CM1037B	1.38**	-4.6**	-6.6**	-0.97**	-0.01**	-31.41**	5.39**	-0.02	-73.52*	0.31**	6.4**	-3.84**
CM1112B	-1.42**	-10.13**	-2.36**	-0.76**	-0.05**	9.87**	-3.66**	0.14**	87.37**	0.12	3.69**	2.09**
CM1162B	1.81**	-2.27**	-1.12**	0.26**	0.01**	-11.98**	-2.96**	0.16**	-61.03	-0.38**	2.73**	-9.84**
CM5032B	0.12	2.01**	6.54**	0.23**	0.02**	32.74**	-1.22*	-0.13**	155.36***	0.12	-4.9**	14.66**
CM5076B	-1.63**	20.33**	5.09**	1.02**	-0.01**	54.06**	0.41	-0.11**	399.63**	0.06	-3.78**	18.88**
CD 95% GCA(Line)	0.54	0.8	0.51	0.04	0.01	3.04	1.01	0.04	61.49	0.17	1.41	1.57
Lines with significantly -ve effects	2	4	4	2	3	4	3	3	2	2	3	3
Lines with significantly +ve effects	1	2	2	4	3	2	2	2	2	1	3	3
<b>Testers</b>												
NCR3295	-1.51**	16.03**	0.32	2.16**	0.04**	19.97**	9.11**	0.2**	578.18**	-0.3**	-30.95**	2.16**
NCR4293	0.49	6.2**	-0.89**	0.48**	-0.03**	-6.21**	4.99**	0.08**	-53.74	-0.12	-22**	4.78**
NCR1681	0.51	21.88**	-0.97**	-2.63**	-0.1**	-5.3**	4.63**	-0.49**	4.81	0.35**	30.76**	-10.36**
NCR1886	0.22	-10.9**	0.7**	-0.12**	0	2.14	-4.87**	0	-34.35	-0.27**	-6.53**	3.72**
NCR1748	1.45**	-15.24**	2.53**	0.22**	0.11**	-0.31	3.67**	0.19**	360.78**	0.12	-2.4**	15.46**
NCR1238	-1.16**	-17.97**	-1.7**	-0.11**	-0.02**	-10.28**	-17.53**	0.01	-124.49**	0.23*	31.13**	-15.76**
CD 95% GCA(Tester)	0.54	0.8	0.51	0.04	0.01	3.04	1.01	0.04	61.49	0.17	1.41	1.57
Testers with significantly -ve effects	3	3	3	3	3	3	2	1	2	2	4	2
Testers with significantly +ve effects	0	3	2	3	2	1	4	3	1	2	2	4

\*: Significant at 5% level; \*\*: significant at 1% level.

**Note:** DFP-Days to 50% flowering, PH- Plant height, PW- Plant width, FL-Fruit length, FW- Fruit width, NFPP-Number of fruit per plant, ASC-Average seed count per fruit, TSW –Thousand seed weight, DCY-Dry chilli yield per plot, LCV- Leaf curl virus tolerance, PUN –Pungency values in Scoville Heat Units mentioned in 1000's, CCL-Capsanthin colour values mentioned in ASTA.

Table 3 : Estimates of specific combining ability effects of 36 crosses for twelve characters in chilli.

S. no.	Crosses	DFP	PH	PW	FL	FW	NFPP	ASC	TSW	DCY	LCV	PUN	CCL
1	CM1008A × NCR3295	2.44**	9**	2.26**	0.27**	0	1.8	8.62**	0.03	204.21**	0.19	-0.88	-29.59**
2	CM1008A × NCR4293	-0.9	3.4**	-3.73**	0.55**	-0.02	1.89	-3.04*	-0.06	136.8	0.43*	-4.22*	4.37*
3	CM1008A × NCR1681	0.67	-4.19**	-4.12**	0.54**	0.06**	7.68*	11.71**	0.03	102.28	-0.21	-2.02	6.68**
4	CM1008A × NCR1886	1.22	-4.08**	-2.26**	-0.54**	-0.05**	-17.09**	-6.81**	0.06	-470.43**	-0.25	-4.03*	0.51
5	CM1008A × NCR1748	-2.77**	-1.87	8.31**	-0.08	0.03**	16.75**	-1.05	-0.19**	540.59**	-0.14	0.6	16.11**
6	CM1008A × NCR1238	-0.66	-2.26*	-0.46	-0.73**	-0.03*	-11.04**	-9.42**	0.12**	-513.45**	0	10.55**	1.91
7	CM1037A × NCR3295	-1.2	-1.13	-1.99**	-0.25**	-0.02	-32.87**	-0.8	-0.19**	-629.33**	0.25	-18.9**	8.16**
8	CM1037A × NCR4293	0.05	-12.14**	0.33	-0.73**	-0.01	25.63**	-0.35	0.11*	318.67**	0.31	-15.44**	4.29*
9	CM1037A × NCR1681	-0.3	10.88**	-5.26**	0.69**	0.1**	-22.27**	1.38	0.1*	273.57**	-0.32	-0.39	-7.57**
10	CM1037A × NCR1886	-0.84	-1.46	6.39**	0.09	-0.08**	30.96**	8.46**	0.06	540.12**	0.3	-3.67*	6.68**
11	CM1037A × NCR1748	0.67	4.94**	-0.73	-0.22**	0.01	-6.42	-4.53**	-0.1*	-500.04**	-0.17	23.32**	11.36**
12	CM1037A × NCR1238	1.62*	-1.09	1.26*	0.43**	0.01	4.98	-4.16**	0.01	-3	-0.37	15.09**	-22.92**
13	CM1112A × NCR3295	1.6*	-1.4	1.24	-0.24**	0.03**	2.59	-1.56	-0.05	-580.38**	-0.98**	0.29	9.9**
14	CM1112A × NCR4293	-0.06	-2.32*	1.26*	-0.63**	0.01	2.02	10.06**	0.04	-381.22**	-0.49*	0.04	-8.72**
15	CM1112A × NCR1681	-0.58	-7.68**	-1.16	0	-0.25**	13.76**	4.34**	-0.27**	953.52**	0.29	-6.79**	-7.34**
16	CM1112A × NCR1886	0.22	5.57**	-0.03	0.65**	0.14**	-16.19**	-12.61**	0.26**	-173.52*	0.58**	-4.02*	-6.84**
17	CM1112A × NCR1748	-1.94**	-1.76	-0.24	-0.32**	0.03*	6.1	-6.16**	0.07	464.07**	0.52*	3.15	3.51
18	CM1112A × NCR1238	0.76	7.6**	-1.06	0.53**	0.05**	-8.27*	5.92**	-0.05	-282.47**	0.08	7.32**	9.48**
19	CM1162A × NCR3295	-0.3	4.47**	-1.28*	0.19**	-0.01	-1.02	5.7**	0.02	-27.9	-0.31	3.24	26.5**
20	CM1162A × NCR4293	-1.97**	-4.91**	-3.97**	0.76**	-0.01	7.34	-8.94**	0.03	47.27	-0.41	8.17**	12.29**
21	CM1162A × NCR1681	-0.81	11.29**	1.26*	-0.54**	0.01	7.81*	8.65**	-0.11*	-657.41**	-0.05	11.73**	-18.32**
22	CM1162A × NCR1886	1.56*	-8.21**	-0.36	-0.1*	-0.02*	-6.34	-7.75**	-0.07	-71.54	-0.5*	6.52**	-4.16*
23	CM1162A × NCR1748	-0.59	0	6.98**	0.22**	0.04**	9.34*	4.24**	-0.01	371.64**	0.61**	10.97**	2.61
24	CM1162A × NCR1238	2.1**	-2.64**	-2.64**	-0.53**	-0.01	-17.14**	-1.9	0.14**	337.94**	0.66**	-40.64**	-18.92**
25	CM5032A × NCR3295	-1.69*	-6.35**	-3.58**	0.12*	0.03**	14.41**	-12.62**	0.23**	758.63**	0.69**	17.96**	-13.5**
26	CM5032A × NCR4293	-0.6	16.98**	2.04**	0.39**	-0.03**	-31.91**	1.33	-0.14**	-262.54**	-0.49*	12.6**	-9.79**
27	CM5032A × NCR1681	3.22**	-17.2**	9.71**	-0.19**	0.06**	-11.08**	-19.47**	0.1*	-583.97**	0.37	3.99*	14.93**
28	CM5032A × NCR1886	0.26	0.92	1.45*	-1.02**	0.01	49.32**	11.11**	0.12**	1063.99**	-0.17	-5.98**	11.93**
29	CM5032A × NCR1748	2.94**	-3.41**	-5.71**	0.3**	-0.05**	-9.65*	17.82**	-0.03	-428.41**	-0.56**	-22.92**	-13.22**
30	CM5032A × NCR1238	-4.12**	9.07**	-3.9**	0.4**	-0.01	-11.09**	1.85	-0.29**	-547.7**	0.16	-5.65**	9.66**

Table 3 continued....

Table 3 continued...

31	CM5076A × NCR3295	-0.85	-4.59**	3.36**	-0.09	-0.04**	15.09**	0.66	-0.04	274.77**	0.16	-1.72	-1.47
32	CM5076A × NCR4293	3.48**	-1.01	4.07**	-0.33**	0.07**	-4.98	0.94	0.01	141.02	0.65**	-1.15	-2.43
33	CM5076A × NCR1681	-2.2**	6.9**	-0.43	-0.5**	0.03*	4.11	-6.61**	0.14**	-88	-0.07	-6.51**	11.62**
34	CM5076A × NCR1886	-2.41**	7.26**	-5.19**	0.93**	0	-40.66**	7.59**	-0.43**	-888.62**	0.05	11.18**	-8.13**
35	CM5076A × NCR1748	1.69*	2.1*	-8.6**	0.1*	-0.05**	-16.12**	-10.31**	0.26**	-447.86**	-0.25	-15.14**	-20.36**
36	CM5076A × NCR1238	0.3	-10.67**	6.8**	-0.1*	-0.01	42.56**	7.72**	0.06	1008.69**	-0.53*	13.34**	20.78**
	<b>CD 95% SCA</b>	1.32	1.96	1.24	0.1	0.02	7.44	2.48	0.09	150.62	0.42	3.45	3.85
Number of crosses with	Significantly -ve effects	7	14	13	16	9	13	13	8	15	6	13	14
	Significantly +ve effects	8	12	13	16	12	11	13	9	13	7	1	16

\*: Significant at 5% level; \*\*: significant at 1% level.

**Note:** DFF-Days to 50% flowering, PH- Plant height, PW- Plant width, FL-Fruit length, FW- Fruit width, NFPP-Number of fruit per plant, ASC-Average seed count per fruit, TSW -Thousand seed weight, DCY-Dry chilli yield per plot, LCV- Leaf curl virus tolerance, PUN -Pungency values in Scoville Heat Units mentioned in 1000's, CCL-Capsanthin colour values mentioned in ASTA.

The *GCA* effects of the parents revealed that the lines CM5076B is a good general combiners for most of the traits like PH, PW, FL, NFPP and DCY exhibiting significant *GCA* effects (table 2). The line CM5076B also showed negative significant *GCA* effects for DFF indicating their usefulness in breeding for early maturing hybrids. The line CM5032B was best general combiner for DCY, PH, PW, FL, FW & NFPP. The line CM1112B was best general combiner for DFF, TSW, DCY, NFPP, PUN & CCL. In case of *GCA* effects, significant *GCA* effect in favourable direction as observed in many lines for DFF(2), PH(2), PW(2), FL(4), FW(3), NFPP(2), ASC(2), TSW(2), DCY(2), LCV(1), PUN(3) and CCL(3) (table 4). The parents, which are good general combiners for yield and yield attributing *GCA* effects in the desired direction for yield components was also comply with the reports of Hasanuzzaman and Faruq (2011), Hasanuzzaman *et al.* (2012), Sharma *et al.* (2013) and Kranthi Rekha *et al.* (2016).

Among the testers, NCR3295 was the best general combiner for majority of the yield component traits i.e., PH, FW, NFPP, ASC, TSW & DCY. It also exhibited significant negative *GCA* effect in a desired direction for DFF. The tester NCR1748 was best general combiner for DCY, FL, FW, PW, ASC & TSW. In case of *GCA* effects, significant *GCA* effect in favourable direction as observed in testers for DFF(3), PH(3), PW(2), FL(3), FW(2), NFPP(1), ASC(4), TSW(3), DCY(1), LCV(2), PUN(2) and CCL(4) (table 4). The parents, which are good general combiners for yield and yield attributing *GCA* effects in the desired direction for yield components was also comply with the reports of Hasanuzzaman and Faruq (2011), Hasanuzzaman *et al.* (2012), Sharma *et al.* (2013) and Kranthi Rekha *et al.* (2016).

Among the lines CM5076B, CM5032B nad CM1112B were proved to be good combiners for dry chilli yield per plot, days to 50% flowering, plant height, plant width, fruit length, fruit width, number of fruits per plant, pungency and capsanthin color values and the testers NCR3295 and NCR1748 were proved to be good combiners for dry chilli yield per plot, days to 50% flowering, plant height, plant width, fruit length, fruit width, number of fruits per plant, average seed count per fruit, thousand seed weight and capsanthin color values.

Twelve crosses were identified as good specific combinations for DCY (table 3). The cross combination CM1162AxNCR1748 showed significant positive SCA effects for PW, FL, FW, NFPP, ASC, DCY, & LCV and cross CM5032A × NCR3295 showed significant positive *GCA* effects for FL, FW, NFPP, TSW, DCY & LCV

**Table 4 :** Promising general combiners identified for yield and yield attributing traits in chilli.

S.no	Parents	No. of characters with favourable GCA effects	Dry chilli yield and yield attributing traits
<b>Lines</b>			
1.	CM5076B	7	Dry chilli yield per plot, Days to 50% flowering, plant height, plant width, fruit length, number of fruits per plant, Capsanthin colour-ASTA
2.	CM5032B	7	Dry chilli yield per plot, Plant height, plant width, fruit length, fruit width, number of fruits per plant, Capsanthin colour-ASTA
3	CM1112B	5	Dry chilli yield per plot, Days to 50% flowering, thousand seed weight, Pungency-SHU and Capsanthin colour value-ASTA
<b>Testers</b>			
4	NCR3295	9	Dry chilli yield per plot, Days to 50% flowering, plant height, fruit length, fruit width, number of fruits per plant, average seed count per fruit, thousand seed weight and Capsanthin colour value-ASTA
5	NCR1748	7	Dry chilli yield per plot, Plant width, fruit length, fruit width, average seed count per fruit, thousand seed weight and Capsanthin colour value-ASTA

**Table 5 :** Promising specific combiners identified for yield and yield attributing traits in chilli.

S. no.	Crosses	Number of characters with favourable SCA effects	Primary character of interest : Dry chilli yield per plot with SCA effects	Other yield attributing characters with desirable SCA effects
1	CM5076A×NCR1238	6	1088.69***	Plant width, number of fruits per plant, average seed count per fruit, pungency and capsanthin colour value
2	CM5032A×NCR1886	6	1063.9***	Plant width, number of fruits per plant, thousand seed weight, average seed count per fruit and capsanthin colour value
3	CM5032A×NCR3295	8	758.63***	Days to 50% flowering, fruit length, fruit width, number of fruits per plant, average seed count per fruit and leaf curl virus tolerance and Pungency-SHU
4	CM1008A×NCR1748	6	540.59***	Days to 50% flowering, Plant width, fruit width, number of fruits per plant and Capsanthin colour-ASTA
5	CM1037A×NCR1886	5	540.12***	Plant width, number of fruits per plant, average seed count per fruit and capsanthin colour value
6	CM1162A×NCR1748	8	371.64***	Plant width, fruit length, fruit width, number of fruits per plant, average seed count per fruit, leaf curl virus tolerance and Pungency-SHU
7	CM1037A×NCR1681	5	273.57***	Plant height, fruit length, fruit width and thousand seed weight
8	CM1008A×NCR3295	5	204.21**	Plant height, Plant width, fruit length and average seed count per fruit

and with a negative significant *SCA* effect for DFF, indicating suitability for early maturing hybrids (table 3). In case of *SCA* effects, significant *SCA* effect in favourable direction as observed in many crosses for DFF(7), PH(12), PW(13), FL(16), FW(12), NFPP(11), ASC(13), TSW(9), DCY(13), LCV(7), PUN(1) and CCL(16) (table 5). These results also getting support from

research reports of Prasath and Ponnuswami (2008), Prajapati and Agalodia (2011) and Kranthi Rekha *et al.* (2016). The crosses CM1112A × NCR1748, CM1112A × NCR1238, CM5076A × NCR1748 and CM1112A × NCR1681 involved parents with high × low *GCA* effects indicating the involvement of additive × dominance genetic interaction. Bhagyalakshmi *et al.* (1991), Nandadevi *et*

**Table 5 :** Parental GCA effects for the superior cross combination.

S. no.	Hybrids	Female	Male	Remarks
1	CM5076AxNCR3295	High GCA	High GCA	
2	CM5076AxNCR1238	High GCA	Low GCA	
3	CM1112AxNCR1748	High GCA	Low GCA	
4	CM1112AxNCR1681	High GCA	Low GCA	
5	CM1008AxNCR3295	Low GCA	High GCA	
6	CM1037AxNCR4293	Low GCA	Low GCA	
7	CM1037AxNCR1681	Low GCA	Low GCA	
8	CM1037AxNCR1886	Low GCA	Low GCA	
9	CM1162AxNCR1748	Low GCA	Low GCA	
10	CM1162AxNCR1238	Low GCA	Low GCA	
11	CM5032AxNCR3295	Low GCA	Low GCA	
12	CM5032AxNCR1886	Low GCA	Low GCA	
13	CM1008AxNCR1748	Low GCA	Low GCA	

*al.* (2003) and Kranthi Rekha *et al.* (2016) also reported about the possibility of interaction between positive alleles from good combiner and negative alleles from poor combiners in high  $\times$  low crosses in chilli. On the other cross combinations CM1008A  $\times$  NCR1748, CM1037A  $\times$  NCR4293, CM1162A  $\times$  NCR1681 and CM5032A  $\times$  NCR1886 involved low  $\times$  low combining parents indicating over dominance and epistatic interactions. The results clearly indicated that the high performance of hybrid need not be the ones with high *SCA* effect and vice versa. Similar results also obtained by Khalil and Hatem (2014), Mendes *et al.* (2014), Suryakumari *et al.* (2014) and Kranthi Rekha *et al.* (2016). In spite of involvement of both poor general combiners in some crosses or one of the parents as poor general combiner, these cross combinations expresses significant *SCA* effects in desirable direction, which might be due to concentrations and interaction between favourable genes contributed by parents. The crosses namely CM5076A  $\times$  NCR3295 is having high  $\times$  high, CM5076A  $\times$  NCR1238, CM1112A  $\times$  NCR1748, CM1112A  $\times$  NCR1681 are having high  $\times$  low and CM1008A  $\times$  NCR3295 is having low  $\times$  high and CM1037A  $\times$  NCR4293, CM1037A  $\times$  NCR1681, CM1037A  $\times$  NCR1886, CM1162A  $\times$  NCR1748, CM1162A  $\times$  NCR1238, CM5032A  $\times$  NCR3295, CM5032A  $\times$  NCR1886, CM1008A  $\times$  NCR1748 are having low  $\times$  low *GCA* (table 6) parental combinations for best specific combiners for characters *viz.*, DCY, FW, PW, NFPP and DFF, which are having high  $\times$  low, and low  $\times$  high and high  $\times$  high *GCA* parental combination, indicating the genetic interaction of the additive and non-additive types.

Based on significant high *SCA* effects, eight hybrids CM5076A  $\times$  NCR1238, CM5032A  $\times$  NCR1886,

CM5032A  $\times$  NCR3295, CM1008A  $\times$  NCR1748, CM1037A  $\times$  NCR1886, CM1162A  $\times$  NCR1748, CM1037A  $\times$  NCR1681 and CM1008A  $\times$  NCR1886 were identified as promising for dry chilli yield per plant and majority of yield attributing characters (table 5). The best specific combination for dry chilli yield per plant is CM5076A  $\times$  NCR1238 recorded highest *SCA* effect of 1088.69 and also recorded the desirable significant *SCA* effects for plant width, number of fruits per plant, average seed count per fruit, pungency and capsanthin colour value. The second best combination for dry chilli yield per plot is CM5032  $\times$  NCR1886 recorded the *SCA* effect of 1063.9 and also recorded the desirable significant *SCA* effects for plant width, number of fruits per plant, thousand seed weight, average seed count per fruit and capsanthin colour value. Whereas the third best cross is CM5032A  $\times$  NCR3295 had significant *SCA* effect of 758.63 and also recorded the desirable significant *SCA* effects for days to 50% flowering, fruit length, fruit width, number of fruits per plant, average seed count per fruit, leaf curl virus tolerance and pungency. The fourth best specific combination is CM1008A  $\times$  NCR1748 had significant *SCA* effect of 540.59 and also recorded desirable significant *SCA* effects for days to 50% flowering, plant width, fruit width, number of fruits per plant and capsanthin colour. The fifth best specific combination is CM1037A  $\times$  NCR1886 had significant *SCA* effect of 540.12 and also recorded desirable significant *SCA* effects for plant width, number of fruits per plant, average seed count per fruit and capsanthin colour value. The sixth best combination is CM1162A  $\times$  NCR1748 had significant *SCA* effect of 371.64 and also recorded the desirable significant *SCA* effects for plant width, fruit length, fruit width, number of fruits per plant, average seed count per fruit, leaf curl



virus tolerance and pungency. The performance of these crosses needs to be critically evaluated over different seasons and locations to confirm their superiority and stability.

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